

# FIG. 1A

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gtgttgctcc actgtcagtc ctccagagcc tcaagagatc tttgggccat atcagctttc 60
tttccaaaat gaacacacccc aggggcagga aagaatgctc tttccttggt cattaagggg 120
cctggggagtc ctggaccagc ttttcatgca gctagaccac ttacatgcaa ctagagcctt 180
gactttgaaa cgaggggacaa aagcatctct tgctaaagggt aactttctgct gcttagaacc 240
cagcctcctc accaccatct gatctatctt gttctcttca caaaaggctc tgaagacatc 300

atg aac cca caa cgg gag gca gca ccc aaa tcc tat gct att cgt gat 348
Met Asn Pro Gln Arg Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp
1 5 10 15

tct cga cag atg gtg tgg gtc ctg agt gga aat tct tta ata gca gct 396
Ser Arg Gln Met Val Trp Val Leu Ser Gly Asn Ser Leu Ile Ala Ala
20 25 30

cct ctt agc cgc agc att aag cct gtc act ctt cat tta ata gcc tgt 444
Pro Leu Ser Arg Ser Ile Lys Pro Val Thr Leu His Leu Ile Ala Cys
35 40 45

aga gac aca gaa ttc agt gac aag gaa aag ggt aat atg gtt tac ctg 492
Arg Asp Thr Glu Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu
50 55 60

gga atc aag gga aaa gat ctc tgt ctc ttc tgt gca gaa att cag ggc 540
Gly Ile Lys Gly Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly
65 70 75 80

aag cct act ttg cag ctt aag gaa aaa aat atc atg gac ctg tat gtg 588
Lys Pro Thr Leu Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val
85 90 95

gag aag aaa gca cag aag ccc ttt ctc ttt ttc cac aat aaa gaa ggc 636
Glu Lys Lys Ala Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly
100 105 110

tcc act tct gtc ttt cag tca gtc tct tac cct ggc tgg ttc ata gcc 684
Ser Thr Ser Val Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala
115 120 125

acc tcc acc aca tca gga cag ccc atc ttt ctc acc aag gag aga ggc 732
Thr Ser Thr Thr Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly
130 135 140

ata act aat aac act aac ttc tac tta gat tct gtg gaa taa 774
Ile Thr Asn Asn Thr Asn Phe Tyr Leu Asp Ser Val Glu
145 150 155

atccagccta ggctgtgggt ggctggttcc aggatagaga atcaagctgt cagagtcac 834
ttaacagatc attatgcgac tgagttcact agcagttcag cccatccata gcttacctca 894

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## FIG. 1B

ttcttactat ccaaaagcca cctcctcctc caaacatcca tttotgtacc aagacctca 954  
ctcgaatgtc actatcccaa gatgaaacct aaaaatcact ttccattctt tcttgatctt 1014  
acccaccat ccactcagct gccatgcca gtttagtta cccccaaat gctgcttcat 1074  
gcaaccttcc attcctattc cttttgcaa cccatgatgt agagatgtgg attcatgaca 1134  
ttttgttcat acaacttctt caataaaaca ttataatatg tgcccaaag ataaagctga 1194  
agaatgagat gaatgtgaaa ttaaaggttt gcatgtcttc ctaatcctaa 1244

# FIG. 2

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1
IL-1_delta -----MNPQ REAAPKSYAI RDSRQMVWVL
IL-1ra-L -----MNPQ REAAPKSYAI RDSRQMVWVL
IL-1_epsilon -----MEKAL KIDTPQQGSI QDINHRVWVL
IL-1ra_sec MEICRGLRSH LITLLFLFLH SETICRPSGR KSSKMQAFRI WDVNQKTFYL
IL-1_beta -----APVRSNLCTL RDSQQKSLVM
consensus -----MNPQ -EAAP-SYAI RDS-Q-VWVL

51
IL-1_delta SG.NSLIAAP LRSIKPVTI HLIACRDTEF SDKEKGNMVY LGIKGDLCCL
IL-1ra-L SG.NSLIAAP LRSIKPVTI HLIACRDTEF SDKEKGNMVY LGIKGDLCCL
IL-1_epsilon QD.QTLIAVP RKDRMSPVTI ALISCRHVET LEKDRGNPIY LGLNGLNLCL
IL-1ra_sec RN.NQLVAGY LQ...GP.NV NLEEKIDVVP IEP...HALF LGIHGGKMCL
IL-1_beta SGPYELKALH LQGQDMEQQV .VFSMSFVQG EESNDKIPVA LGLKEKNLYL
consensus SG-NSLIAAP L-RSIKPVT- HLI-CRDVEF SEKEKGN-VY LGIKGD-LCL

101
IL-1_delta FCAEIQGKPT LQLKLQGSQD .NIGKDTCKW LVGIHTCINL DVRESCFMG.
IL-1ra-L FCAEIQGKPT LQLKEKNIMD LYVEKKAQKP FLFFH...NK EGSTSVFQSV
IL-1_epsilon MCAKVGDOPT LQLKEKDIMD LYNQPEPVKS FLFYH...SQ SGRNSTFESV
IL-1ra_sec SCVKSGDETR LQLEAVNITD LSENKQDKR FAFIR...SD SGPTTSFESA
IL-1_beta SCVLKDDKPT LQLESVDPKN .YPKKKMEKR FVFNKIEINN KLE...FESA
consensus -CA-I-DKPT LQLKE--IMD LY--KK--KR F-FIH--IN- SGRTS-FES-

151
IL-1_delta TLDQWGIGVG RKKWKSSFQH HHLRKKDKDF SSMRTNIGMP GRM
IL-1ra-L SYPGWFIATS TTSGQPIF...LTKEGI TN.NTNFYLD SVE
IL-1_epsilon AFGWFIATS SEGGCPLILT QELGKANTTD FGLTMLF----
IL-1ra_sec ACPGWFLCTA MEADQPVSLT N...MPDEGV MVTKFYFQED E--
IL-1_beta QFPNWIYISTS QAENMPVFLG GTKGGQDITD FTMQFVSS--
consensus AFGWFIATS -E-GQPVFLT --LGKKD--D F-M--NF--D ---

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